AU 1806

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/231,565A*

DATE: 05/01/96
TIME: 11:15:20

INPUT SET: S10230.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

```
 1                          SEQUENCE LISTING
 2
 3   (1)      General Information:
 4
 5        (i)       APPLICANTS:  KAWAKAMI, YUTAKA; ROSENBERG,
 6                  STEVEN A.
 7
 8        (ii)      TITLE OF INVENTION: MELANOMA ANTIGENS AND
 9                  THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
10                  METHODS
11
12        (iii)     NUMBER OF SEQUENCES:  43
13
14        (iv)      CORRESPONDENCE ADDRESS:
15                  (A)   ADDRESSEE:  MORGAN & FINNEGAN
16                  (B)   STREET:  345 PARK AVENUE
17                  (C)   CITY:  NEW YORK
18                  (D)   STATE:  NEW YORK
19                  (E)   COUNTRY:  USA
20                  (F)   ZIP:  10154
21
22        (v)       COMPUTER READABLE FORM:
23                  (A)   MEDIUM TYPE:  FLOPPY DISK
24                  (B)   COMPUTER:  IBM PC COMPATIBLE
25                  (C)   OPERATING SYSTEM:  PC-DOS/MS-DOS
26                  (D)   SOFTWARE:  ASCII
27
28        (vi)      CURRENT APPLICATION DATA:
29                  (A)   APPLICATION NUMBER:  08/231,565
30                  (B)   FILING DATE:  22-APR-1994
31                  (C)   CLASSIFICATION:
32
33        (viii)    ATTORNEY/AGENT INFORMATION:
34                  (A)   NAME: CAROL M. GRUPPI
35                  (B)   REGISTRATION NUMBER: 37,341
36                  (C)   REFERENCE/DOCKET NUMBER:  2026-4124
37
38        (ix)      TELECOMMUNICATION INFORMATION:
39                  (A)   TELEPHONE:  (212) 758-4800
40                  (B)   TELEFAX:  (212) 751-6849
41                  (C)   TELEX:  421792
42
43   (2) INFORMATION FOR SEQ ID NO:1:
44
45        (i) SEQUENCE CHARACTERISTICS:
46                  (A) LENGTH:  1559
```

```
47              (B) TYPE:  NUCLEOTIDE
48              (C) STRANDEDNESS:  DOUBLE
49              (D) TOPOLOGY:  UNKNOWN
50
51        (ii) MOLECULE TYPE:  cDNA
52
53
54
55
56
57
58
59
60        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62
63    AGCAGACAGA GGACTCTCAT TAAGGAAGGT GTCCTGTGCC              40
64
65    CTGACCCTAC AAGATGCCAA GAGAAGATGC TCACTTCATC              80
66
67    TATGGTTACC CCAAGAAGGG GCACGGCCAC TCTTACACCA             120
68
69    CGGCTGAAGA GGCCGCTGGG ATCGGCATCC TGACAGTGAT             160
70
71    CCTGGGAGTC TTACTGCTCA TCGGCTGTTG GTATTGTAGA             200
72
73    AGACGAAATG GATACAGAGC CTTGATGGAT AAAAGTCTTC             240
74
75    ATGTTGGCAC TCAATGTGCC TTAACAAGAA GATGCCCACA             280
76
77    AGAAGGGTTT GATCATCGGG ACAGCAAAGT GTCTCTTCAA             320
78
79    GAGAAAAACT GTGAACCTGT GGTTCCCAAT GCTCCACCTG             360
80
81    CTTATGAGAA ACTCTCTGCA GAACAGTCAC CACCACCTTA             400
82
83    TTCACCTTAA GAGCCAGCGA GACACCTGAG ACATGCTGAA             440
84
85    ATTATTTCTC TCACACTTTT GCTTGAATTT AATACAGACA             480
86
87    TCTAATGTTC TCCTTTGGAA TGGTGTAGGA AAAATGCAAG             520
88
89    CCATCTCTAA TAATAAGTCA GTGTTAAAAT TTTAGTAGGT             560
90
91    CCGCTAGCAG TACTAATCAT GTGAGGAAAT GATGAGAAAT             600
92
93    ATTAAATTGG GAAAACTCCA TCAATAAATG TTGCAATGCA             640
94
95    TGATACTATC TGTGCCAGAG GTAATGTTAG TAAATCCATG             680
96
97    GTGTTATTTT CTGAGAGACA GAATTCAAGT GGGTATTCTG             720
98
99    GGGCCATCCA ATTTCTCTTT ACTTGAAATT TGGCTAATAA             760
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100
101    CAAACTAGTC AGGTTTTCGA ACCTTGACCG ACATGAACTG                800

102
103    TACACAGAAT TGTTCCAGTA CTATGGAGTG CTCACAAAGG                840

104
105    ATACTTTTAC AGGTTAAGAC AAAGGGTTGA CTGGCCTATT                880

106
107    TATCTGATCA AGAACATGTC AGCAATGTCT CTTTGTGCTC                920

108
109    TAAAATTCTA TTATACTACA ATAATATATT GTAAAGATCC                960

110
111
112
113
114
115
116
117
118    TATAGCTCTT TTTTTTTGAG ATGGAGTTTC GCTTTTGTTG                1000

119
120    CCCAGGCTGG AGTGCAATGG CGCGATCTTG GCTCACCATA                1040

121
122    ACCTCCGCCT CCCAGGTTCA AGCAATTCTC CTGCCTTAGC                1080

123
124    CTCCTGAGTA GCTGGGATTA CAGGCGTGCG CCACTATGCC                1120

125
126    TGACTAATTT TGTAGTTTTA GTAGAGACGG GGTTTCTCCA                1160

127
128    TGTTGGTCAG GCTGGTCTCA AACTCCTGAC CTCAGGTGAT                1200

129
130    CTGCCCGCCT CAGCCTCCCA AAGTGCTGGA ATTACAGGCG                1240

131
132    TGAGCCACCA CGCCTGGCTG GATCCTATAT CTTAGGTAAG                1280

133
134    ACATATAACG CAGTCTAATT ACATTTCACT TCAAGGCTCA                1320

135
136    ATGCTATTCT AACTAATGAC AAGTATTTTC TACTAAACCA                1360

137
138    GAAATTGGTA GAAGGATTTA AATAAGTAAA AGCTACTATG                1400

139
140    TACTGCCTTA GTGCTGATGC CTGTGTACTG CCTTAAATGT                1440

141
142    ACCTATGGCA ATTTAGCTCT CTTGGGTTCC CAAATCCCTC                1480

143
144    TCACAAGAAT GTGCAGAAGA AATCATAAAG GATCAGAGAT                1520 ·

145
146    TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAA                 1559

147
148 ·
149    (2) INFORMATION FOR SEQ ID NO:2:

150
151          (i) SEQUENCE CHARACTERISTICS:
152                (A) LENGTH:  118
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```
153                    (B) TYPE:  amino acid
154                    (C) STRANDEDNESS:  Unknown
155                    (D) TOPOLOGY:  Unknown
156
157         (ii) MOLECULE TYPE:  Protein
158
159         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
160
161
162    Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys
163    1               5                  10
164
165    Lys Gly His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala
166    15              20                 25
167
168
169
170
171
172
173
174
175    Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu Leu
176        30              35                 40
177
178    Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala
179            45              50                 55
180
181    Leu Met Asp Lys Ser Leu His Val Gly Thr Gln Cys Ala Leu
182            60                  65                 70
183
184    Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp His Arg Asp Ser
185                75                  80
186
187    Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val Val Pro
188    85                  90                 95
189
190    Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
191        100                 105                110
192
193    Pro Pro Pro Tyr Ser Pro
194            115
195
196
197    (2) INFORMATION FOR SEQ ID NO:3:
198
199         (i) SEQUENCE CHARACTERISTICS:
200                    (A) LENGTH:  9
201                    (B) TYPE:  amino acid
202                    (C) STRANDEDNESS:  Unknown
203                    (D) TOPOLOGY:  Unknown
204
205         (ii) MOLECULE TYPE:  Peptide
```

```
206
207          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
208
209
210   Thr Thr Ala Glu Glu Ala Ala Gly Ile
211    1               5
212
213
214   (2) INFORMATION FOR SEQ ID NO:4:
215
216          (i) SEQUENCE CHARACTERISTICS:
217                 (A) LENGTH:  9
218                 (B) TYPE:  amino acid
219                 (C) STRANDEDNESS:  Unknown
220                 (D) TOPOLOGY:  Unknown
221
222          (ii) MOLECULE TYPE:  Peptide
223
224          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
225
226
227
228
229
230
231
232
233   Ala Ala Gly Ile Gly Ile Leu Thr Val
234    1               5
235
236
237   (2) INFORMATION FOR SEQ ID NO:5:
238
239          (i) SEQUENCE CHARACTERISTICS:
240                 (A) LENGTH:  9
241                 (B) TYPE:  amino acid
242                 (C) STRANDEDNESS:  Unknown
243                 (D) TOPOLOGY:  Unknown
244
245          (ii) MOLECULE TYPE:  Peptide
246
247          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
248
249
250   Gly Ile Gly Ile Leu Thr Val Ile Leu
251    1               5
252
253
254   (2) INFORMATION FOR SEQ ID NO:6:
255
256          (i) SEQUENCE CHARACTERISTICS:
257                 (A) LENGTH:  9
258                 (B) TYPE:  amino acid
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/231,565A*

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